

OM nucleic - nucleic search, using sw model

Run on: March 7, 2007, 12:57:57 ; Search time 567 Seconds
(without alignments)
653.489 Million cell updates/sec

Title: US-10-751-113-3

Perfect score: 50
Sequence: 1 tgcacgtgataccaccaga.....actattccaatgatgatga 50

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0.

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 1124038

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*
15: Geneseqn2006s:*
16: Geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	50	ABX11900	ABX11900 Human AIB

2	27.8	55.6	4239	14	ADV43475	Adv43475 Human psy
3	27.8	55.6	4263	12	ADU92834	Adi92834 Human co-
4	27.8	55.6	4495	14	AEH82913	Aec82913 Breast ca
5	27.8	55.6	4789	2	AAK80992	Aax80992 Human sce
6	27.8	55.6	6754	4	AAZ6490	Aat6490 Human SRC
7	27.8	55.6	6754	10	ADK67037	Adk67037 Gene #127
8	27.8	55.6	6754	14	ADY15855	Ady15855 DNA encod
9	27.8	55.6	6754	14	ADY16113	Ady16113 DNA encod
10	27.8	55.6	6754	14	ADY16117	Ady16117 DNA encod
11	27.8	55.6	6832	6	AAJ04039	Aad04039 Human amp
12	27.8	55.6	6835	2	AAV99915	Aav99915 AIB1 (Amp
13	27.8	55.6	6835	14	ADY19927	Ady19927 DNA encod
14	27.8	55.6	6835	14	AEH18120	Aed18120 Fibrotic
15	27.8	55.6	6845	10	ADE76189	Ad76189 Human AIB
16	27.8	55.6	7088	15	AEF22148	Aef22148 Human bas
17	27.8	55.6	7116	10	ADE53851	Ade53851 Human pro
18	27.8	55.6	7923	15	AEH88178	Aeh88178 Human nuc
19	27.8	55.6	7935	15	AEH88176	Aeh88176 Human nuc
20	27.8	55.6	7994	14	ADY16115	Ady16115 DNA encod
21	27.8	55.6	8207	10	ADP81691	Adp81691 Leukaemia
22	27.8	55.6	8207	10	ADP81690	Adp81690 Leukaemia
23	27.8	55.6	12414	14	AEH47654	Aeh47654 Nucleotid
24	27.6	55.2	34	8	ABX11899	Abx11899 Human AIB
25	26.4	52.8	403	9	ACH16713	Ach16713 Human adu
26	26.4	52.8	86453	14	ADY25730	Ady25730 SULF rela
27	26.4	52.8	264965	12	ADN16203	Adn16203 Human sul
28	26.4	52.8	26885	6	ABS56563	Abs56563 Human SUL
29	26.2	52.4	4621	2	AAV99919	Aav99919 Murine p/
30	26.2	52.4	4660	2	AAK26000	Aax26000 Murine p/
31	25	50.0	35	8	ABX11898	Abx11898 Human AIB
32	24.8	49.6	888	13	ADB63401	Adb63401 Cotton CD
33	24.4	48.8	1179	4	AAK87368	Aak87368 Human imm
34	24.4	48.8	3361	2	AAK80993	Aax80993 Mouse sce
35	24.4	48.8	171936	6	ABS56565	Abs56565 Human SUL
36	24.4	48.8	171936	12	ADN16205	Adn16205 Mouse sul
37	24.2	48.4	1664	4	AAF74192	Aaf74192 DNA encod
38	24.2	48.4	110000	14	AEH39174_07	Continuation (8 of
39	24.2	48.4	110000	14	AEH42737_12	Continuation (13 o
40	23.8	47.6	864	8	ACA36808	Aca36808 Prokaryot
41	23.8	47.6	10199	6	ABQ71072	Abq71072 Listeria
42	23.8	47.6	44528	6	ABA03041_29	Continuation (30 o
43	23.8	47.6	169659	12	ADQ59434	Adq59434 Human can
44	23.8	47.6	187851	14	ADQ13735	Adq13735 Human can
45	23.6	47.2	11614	14	AEH61172	Aeh61172 Human HRA

ALIGNMENTS

RESULT 1	ABX11900	standard; cDNA, 50 BP.
ID	ABX11900	
XX	ABX11900	
AC	ABX11900	
XX	ABX11900	
DT	16-MAY-2003	(first entry)
XX		

DE Human AIB1 delta3 isoform mRNA exon 2/exon 4 junction.

XX Human; ss: exon 2/exon 4 junction; amplified in breast cancer;

KW Chromosome 20q; transcription factor; antisense gene therapy; transgenic;

KW siRNA; small inhibitory RNA; cytosolic; intestinal cancer;

KW head and neck cancer; metastatic tissue cancer; neuroblastoma;

KW ovarian cancer; pancreatic cancer; prostate cancer; stomach cancer;

KW breast cancer; AIB1 delta3 isoform.

XX Homo sapiens.

OS

XX MO2003003904-A2.

PN 16-JAN-2003.

PD

XX 03-JUL-2002; 2002MO-US021066.

PF

XX 05-JUL-2001; 2001US-0302648P.

PR (GEOU) UNIV GEORGETOWN MEDICAL CENT.

PA

XX Riegel AT, Reiter R, Wellstein A;

PI Riegel AT, Reiter R, Wellstein A;

XX WPI: 2003-221517/21.

DR

XX New isolated AIB1 isoform as co-activator that potentiates

PT transcriptional activity of nuclear hormone receptors, useful for the

PT diagnosis, prevention and/or treatment of cancers, in particular breast

PT cancer.

XX

PS Example 6; Fig 9; 47pp; English.

XX

CC The invention relates to an isolated isoform of an amplified in breast

CC cancer 1 (AIB1) transcriptional co-activator. Also included are an

CC isolated nucleic sequences that encodes the isoform, a vector that

CC contains the nucleic acid, a recombinant cell that contains the nucleic

CC acid, a diagnostic kit for the detection of cancer (comprising chemical

CC substances that are specifically reactive to the AIB1 isoform or the

CC nucleic acid), an anti-AIB1 isoform antibody (or antibody fragment),

CC detection of cancer in a patient (comprising contacting a biological

CC sample obtained from the patient with at least one chemical substance

CC that specifically binds to the AIB1 isoform or the nucleic acid, and

CC detecting binding), a pharmaceutical composition (comprising an agent

CC that specifically binds to the AIB1 isoform, and prevents a co-activation

CC of a transcription factor when administered to a patient), an siRNA

CC (small inhibitory RNA) that inhibits expression of a transcriptional co-

CC activator protein, a transgenic animal comprising a recombinant gene that

CC encodes the AIB1 isoform and creating the transgenic animal. The

CC compositions comprising the AIB1 isoform or nucleic acids that bind to

CC the AIB1 isoform, are useful for the diagnosis, prevention and/or

CC treatment of disorders associated with the co-activator isoforms, such as

CC cancers of the intestines, head and neck, metastatic tissue,

CC neuroblastoma, ovaries, pancreas, prostate, stomach, and in particular

CC cancer of the breast. The gene for AIB1 is located on chromosome 20q. The

CC present sequence is the junction region of the AIB1 delta3 isoform mRNA

CC for exons 2 and 4 (unique to the delta3 isoform), which was targeted by

CC an siRNA

XX

XX Sequence 50 BP; 18 A; 9 C; 11 G; 12 T; 0 U; 0 Other;

XX

XX Query Match 100.0%; Score 50; DB 8; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 3.2e-09;

XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

DB 1 TGGCATGTGATCTCCAGACAGGAGAAACGATTTCGAATGATGA 50

1 TGGCATGTGATCTCCAGACAGGAGAAACGATTTCGAATGATGA 50

RESULT 2

ADV43475

ID ADV43475 standard; CDNA: 4239 BP.

XX

XX ADV43475;

AC

XX 10-MAR-2005 (first entry)

DT

XX Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1103.

DE

XX

XX microarray; psychoneuroendocrinimmune; chronic fatigue;

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;

KW cancer; neoplasm; infection; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN MO2004108899-A2.

PD

XX 16-DEC-2004.

PF

XX 04-JUN-2004; 2004MO-US017686.

PR

XX 04-JUN-2003; 2003US-0475915P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Nicholson A, Vernon SD;

XX

DR WPI: 2005-031682/03.

XX

PT New microarray comprising probes for genes involved in

PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a

PT condition associated with PNI activity, e.g., inflammatory or infectious

PT diseases.

XX

PS Claim 1; SEQ ID NO 1103; 254pp; English.

XX

XX The invention relates to a new microarray which comprises probes for

CC genes involved in psychoneuroendocrinimmune (PNI) activity. The

CC microarray is useful in diagnosing a condition associated with PNI

CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,

CC cancer and infection. The present sequence represents a

CC psychoneuroendocrinimmune gene expressed sequence tag. Note the

CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2007, 13:22:36 ; Search time 2477 Seconds
(without alignments)
1395.242 Million cell updates/sec

Title: US-10-751-113-3

Perfect score: 50

Sequence: 1 tgcacatgcatcactccagga.....actattcccatgatgata 50

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	27.8	55.6	480	2	CQ712958		CQ712958 Sequence
2	27.8	55.6	4495	2	CS162240		CS162240 Sequence

3	27.8	55.6	4495	5	AF010227	AF010227 Homo sapi
4	27.8	55.6	4668	5	AF016031	AF016031 Homo sapi
5	27.8	55.6	4807	5	BC092516	BC092516 Homo sapi
6	27.8	55.6	5256	5	AB209863	AB209863 Homo sapi
7	27.8	55.6	6754	2	AX821998	AX821998 Homo sapi
8	27.8	55.6	6754	2	BD131717	BD131717 Antisense
9	27.8	55.6	6754	2	CS032155	CS032155 Sequence
10	27.8	55.6	6754	2	CS032413	CS032413 Sequence
11	27.8	55.6	6754	2	CS032417	CS032417 Sequence
12	27.8	55.6	6754	2	CS041107	CS041107 Sequence
13	27.8	55.6	6754	2	CS041365	CS041365 Sequence
14	27.8	55.6	6754	2	CS041369	CS041369 Sequence
15	27.8	55.6	6754	2	CS050236	CS050236 Sequence
16	27.8	55.6	6754	2	DD219303	DD219303 GENE EXP
17	27.8	55.6	6754	2	AR086661	AR086661 Sequence
18	27.8	55.6	6754	5	AF036892	AF036892 Homo sapi
19	27.8	55.6	6755	2	CQ730100	CQ730100 Sequence
20	27.8	55.6	6832	2	AX384818	AX384818 Sequence
21	27.8	55.6	6835	2	BD192354	BD192354 Sequence
22	27.8	55.6	6835	2	AR116837	AR116837 Sequence
23	27.8	55.6	6835	2	CS036227	CS036227 Sequence
24	27.8	55.6	6835	2	CS045179	CS045179 Sequence
25	27.8	55.6	6835	5	AF012108	AF012108 Homo sapi
26	27.8	55.6	7433	5	BC119901	BC119901 Homo sapi
27	27.8	55.6	7433	5	BC122547	BC122547 Homo sapi
28	27.8	55.6	7994	2	CS032415	CS032415 Sequence
29	27.8	55.6	7994	2	CS041367	CS041367 Sequence
30	27.8	55.6	8207	2	AX780089	AX780089 Sequence
31	27.8	55.6	8207	2	AX780090	AX780090 Sequence
32	27.6	55.2	80086	4	AP003290	AP003290 Oryza sat
33	27.6	55.2	88558	4	CNS07YFG	AL713935 Oryza sat
34	27.6	55.2	90750	4	AP003197	AP003197 Oryza sat
35	27.6	55.2	110000	4	AP008209_209	Continuation (210
36	27.6	55.2	110000	4	AP008209_210	Continuation (211
37	27.6	55.2	110000	4	AP008210_134	Continuation (135
38	27.6	55.2	110000	4	AP008210_147	Continuation (148
39	27.6	55.2	110000	4	AP008211_029	Continuation (130 o
40	27.6	55.2	110000	4	AP008211_099	Continuation (1100
41	27.6	55.2	110000	4	AP008215_152	Continuation (153
42	27.6	55.2	110000	4	AP008216_091	Continuation (92 o
43	27.6	55.2	110000	4	AP008218_067	Continuation (68 o
44	27.6	55.2	110000	4	AP008218_195	Continuation (136
45	27.6	55.2	110000	4	AP008218_213	Continuation (214

ALIGNMENTS

RESULT 1	CQ712958	480 bp	DNA
LOCUS	CQ712958		
DEFINITION	Sequence 57884 from Patent WO2070737.		
ACCESSION	CQ712958		
VERSION	CQ712958.1	GI:42273815	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

linear PAT 03-FEB-2004

OM nucleic - nucleic search, using sw model

Run on: March 7, 2007, 13:32:22 ; Search time 5206 Seconds
(without alignments)
595.861 Million cell updates/sec

Title: US-10-751-113-3

Perfect score: 50
Sequence: 1 tgcacatgcatcactccagga.....actatttccaatgatgatga 50

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*
15: gb_est16:*
16: gb_est17:*
17: gb_est18:*
18: gb_est19:*
19: gb_est20:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result % Query SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	28.2	56.4	499	19	CT346760	CT346760 Sus scrofa
2	27.8	55.6	230	5	BK43165	BK43165 DfP2P781P
3	27.8	55.6	531	14	DB070018	DB070018
4	27.8	55.6	532	14	DB060916	DB060916 DB060916
5	27.8	55.6	537	3	BM146766	BM146766 TCNAP1E73
6	27.8	55.6	545	14	DB071966	DB071966 DB071966
7	27.8	55.6	546	14	DA375387	DA375387 DA375387
8	27.8	55.6	556	14	DB091786	DB091786 DB091786
9	27.8	55.6	557	14	DB134417	DB134417 DB134417
10	27.8	55.6	566	14	DA328439	DA328439 DA328439
11	27.8	55.6	574	14	DB067714	DB067714 DB067714
12	27.8	55.6	581	4	BP353331	BP353331 BP353331
13	27.8	55.6	581	4	BP353869	BP353869 BP353869
14	27.8	55.6	582	4	BP280749	BP280749 BP280749
15	27.8	55.6	583	4	BP282535	BP282535 BP282535
16	27.8	55.6	583	4	BP310850	BP310850 BP310850
17	27.8	55.6	583	4	BP315317	BP315317 BP315317
18	27.8	55.6	588	14	DA189529	DA189529 DA189529
19	27.8	55.6	597	14	DA248756	DA248756 DA248756
20	27.8	55.6	609	1	AL698932	AL698932 DfP2P686F
21	27.8	55.6	665	13	DR005834	DR005834 TC116022
22	27.8	55.6	843	8	CD657296	CD657296 AGENCOURT
23	27.6	55.2	399	9	CT538130	CT538130 CT538130
24	27.6	55.2	417	9	CT540319	CT540319 CT540319
25	27.6	55.2	433	9	CT643011	CT643011 CT643011
26	27.6	55.2	908	19	AG891620	AG891620 Oryza sat
27	26.8	53.6	700	7	BB865389	BB865389 BB865389
28	26.6	53.2	668	18	DU475651	DU475651 109841573
29	26.4	52.8	718	2	BF270756	BF270756 CA_EB000
30	26.2	52.4	294	13	DN626023	DN626023 UI-M-EX0-
31	26.2	52.4	394	7	AM153178	AM153178 6636h11.Y
32	26.2	52.4	443	8	CF165306	CF165306 B0754H03-
33	26.2	52.4	469	9	CN682253	CN682253 E0161G12-
34	26.2	52.4	581	9	CN682136	CN682136 E0160C01-
35	26.2	52.4	637	7	BB659498	BB659498 BB659498
36	26.2	52.4	660	5	BY751007	BY751007 BY751007
37	26.2	52.4	672	7	BB865764	BB865764 BB865764
38	26.2	52.4	716	8	CB522550	CB522550 UI-M-GH0-
39	26.2	52.4	1960	6	AK137507	AK137507 Mus muscu
40	26.2	52.4	3923	6	AK156345	AK156345 Mus muscu
41	26.2	52.4	5131	6	AK142306	AK142306 Mus muscu
42	26.2	52.4	5237	6	BC086482	BC086482 Mus muscu
43	26	52.0	424	2	BF887288	BF887288 CP4-TN014
44	25.8	51.6	714	7	BB648365	BB648365 BB648365
45	25.8	51.6	721	2	BF215672	BF215672 601881152

ALIGNMENTS

RESULT 1
LOCUS CT346760 499 bp DNA linear GSS 03-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-41J6, genomic survey sequence.
ACCESSION CT346760

VERSION CT346760.1 GI:79916147
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae; Sus.

REFERENCE 1 (bases 1 to 499)
 HUMPHRAY, S.J., PLUMB, R.W. and DURHAM, J.L.
 Direct Submission
 Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the SP6 end of BAC 41J6. 41J6 is part of the CHORI-242 BAC Library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.

FEATURES
 source
 1..499
 /organism="Sus scrofa"
 /mol_type="genomic DNA"
 /db_xref="taxon:9623"
 /clone="CH242-41J6"
 /issue_type="White blood cells"
 /note="vector pTARBAC1.3_BamHI sex female"

ORIGIN
 Query Match 56.4%; Score 28.2; DB 19; Length 499;
 Best Local Similarity 80.5%; Pred. No. 34;
 Matches 33; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy 10 ATATCCGAGCAGGAGGAAAACTATTTCCATGATGATGA 50
 |||||
 Db 361 ATATCCGAGCAGGAGGAAAACTATTTCCATGATGATGA 401

RESULT 2
 LOCUS BX643165 230 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZP781P1622_r1 781 (synonym: h1cc4) Homo sapiens cDNA clone
 DKFZP781P1622 5', mRNA sequence.
 ACCESSION BX643165
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 230)
 KOEHLER, K., BEYER, A., MEWES, H.W., WEIL, B., AMID, C., OSANGER, A., FOBO, G., HAN, M. and MIEMANN, S.
 EST (KoeHLer, K., Beyer, A., Mewes, H.W., weil, B., Amid, C., et al.)
 Unpublished (2003)
 JOURNAL Contact: MIPS
 PUBMED MIPS
 COMMENT Ingolstaedter Landstr.1, D-85764 Neuberg, Germany

This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ). Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Dusseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No si sequence available. This clone (DKFZP781P1622) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..230
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP781P1622"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="781 (synonym: h1cc4)"
 /note="vector: pSport1_Sfi; site_1: SfiIA; site_2: SfiIB; cDNA-collection"

ORIGIN
 Query Match 55.6%; Score 27.8; DB 5; Length 230;
 Best Local Similarity 82.1%; Pred. No. 42;
 Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 12 ACTCCAGCAGCAGGAGGAAAACTATTTCCATGATGATGA 50
 |||||
 Db 104 ATATAAGCAGCAGGAGGAAAACTATTTCCATGATGATGA 142

RESULT 3
 LOCUS DB070018 531 bp mRNA linear EST 12-MAY-2006
 DEFINITION DB070018 TEST14 Homo sapiens cDNA clone TEST14012418 5', mRNA sequence.
 ACCESSION DB070018
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 531)
 KIMURA, K., WAKAMATSU, A., SUZUKI, Y., OCA, T., NISHIKAWA, T., YAMASHITA, R., YAMAMOTO, J., SEKINE, M., TAITANI, K., WAKAGURI, H., ISHII, S., SUGIYAMA, T., SAITO, K., ISONO, Y., IRIE, R., KUSHIDA, N., YONEYAMA, T., OTSUKA, R., KANDA, K., YOKOI, T., KONDO, H., WAGATSUMA, M., MURAKAWA, K., ISHIDA, S., ISHIBASHI, T., TAKAHASHI-FUJII, A., TANASE, T., NAGAI, K., KIKUCHI, H., NAKAI, K., ISOGLI, T. and SUGANO, S.
 Identification and Characterization of Putative Alternative Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 JOURNAL Contact: Takao Isegaki
 PUBMED 16344560
 COMMENT

OM nucleic - nucleic search, using sw model

Run on: March 7, 2007, 14:13:51 ; Search time 155 Seconds
(without alignments)

603.583 Million cell updates/sec

Title: US-10-751-113-3

Sequence: 1 tgcacatgatcaccacagga.....actattccatgatgatga 50

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7.COMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H.COMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCUS.COMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP.COMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE.COMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.8	55.6	6760	US-09-949-016-4981	Sequence 4981, Ap
2	27.8	55.6	6835	US-09-125-635-1	Sequence 1, Appl
3	26.4	52.8	15782	US-09-949-016-16723	Sequence 16723, A
4	26.2	52.4	4621	US-09-125-635-9	Sequence 9, Appl
5	26.2	52.4	4860	US-09-445-353E-1	Sequence 1, Appl
6	24.2	46.4	524032	US-09-949-016-16928	Sequence 16928, A
7	24.2	48.4	524032	US-09-949-016-16929	Sequence 16929, A

ALIGNMENTS

RESULT 1
US-09-949-016-4981
; Sequence 4981, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEROF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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C	9	24.2	48.4	524032	3	US-09-949-016-16931	Sequence 16931, A
C	10	24.2	48.4	529885	3	US-09-949-016-14340	Sequence 14340, A
C	11	24.2	48.4	529885	3	US-09-949-016-14341	Sequence 14341, A
C	12	24.2	48.4	529885	3	US-09-949-016-14342	Sequence 14342, A
C	13	24.2	48.4	529885	3	US-09-949-016-14343	Sequence 14343, A
C	14	24.2	48.4	529885	3	US-09-949-016-14344	Sequence 14344, A
C	15	24.2	48.4	529885	3	US-09-949-016-14345	Sequence 14345, A
C	16	24.2	48.4	529885	3	US-09-949-016-14346	Sequence 14346, A
C	17	24.2	48.4	529885	3	US-09-949-016-14347	Sequence 14347, A
C	18	23.8	47.6	152582	3	US-09-949-016-12086	Sequence 12086, A
C	19	23.8	47.6	152583	3	US-09-949-016-11790	Sequence 17390, A
C	20	23.8	47.6	152583	3	US-09-949-016-11791	Sequence 17391, A
C	21	22.8	45.6	5143	3	US-09-620-1120-3	Sequence 3, Appl
C	22	22.8	45.6	148783	3	US-09-949-016-15729	Sequence 15729, A
C	23	22.8	45.6	331814	3	US-09-949-016-12008	Sequence 12008, A
C	24	22.8	45.6	331814	3	US-09-949-016-117056	Sequence 17056, A
C	25	22.6	45.2	7011	3	US-09-268-163-9	Sequence 9, Appl
C	26	22.6	45.2	7011	5	US-10-033-026-9	Sequence 9, Appl
C	27	22.4	44.8	601	3	US-09-949-016-61449	Sequence 61449, A
C	28	22.4	44.8	601	3	US-09-949-016-67687	Sequence 67687, A
C	29	22.4	44.8	1194	3	US-10-243-468-1	Sequence 1, Appl
C	30	22.4	44.8	2065	4	US-10-094-749-1293	Sequence 1293, Ap
C	31	22.4	44.8	163181	3	US-09-949-016-13730	Sequence 13730, A
C	32	22.4	44.8	206433	3	US-09-949-016-13527	Sequence 13527, A
C	33	22.4	44.8	254778	3	US-09-949-016-12417	Sequence 12417, A
C	34	22.2	44.4	601	3	US-09-949-016-182740	Sequence 182740, A
C	35	22.2	44.4	1689	3	US-09-247-155-61	Sequence 61, Appl
C	36	22.2	44.4	1689	3	US-09-903-190-61	Sequence 61, Appl
C	37	22.2	44.4	1746	3	US-08-951-130-5	Sequence 5, Appl
C	38	22.2	44.4	1746	3	US-09-430-806A-5	Sequence 5, Appl
C	39	22.2	44.4	1660	3	US-08-895-652A-4	Sequence 4, Appl
C	40	22.2	44.4	2607	2	US-08-369-796-5	Sequence 5, Appl
C	41	22.2	44.4	2607	2	US-08-852-091-5	Sequence 5, Appl
C	42	22.2	44.4	2607	2	US-08-820-754-5	Sequence 5, Appl
C	43	22.2	44.4	2607	3	US-08-956-652-5	Sequence 5, Appl
C	44	22.2	44.4	2607	3	US-08-956-869-5	Sequence 5, Appl
C	45	22.2	44.4	2607	3	US-08-948-547-5	Sequence 5, Appl

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4981
; LENGTH: 6760
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4981

Query Match 55.6%; Score 27.8; DB 3; Length 6760;
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RESULT 2

US-09-125-635-1
; Sequence 1, Application US/09125635
; Patent No. 6562589

GENERAL INFORMATION:

; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1

Query Match 55.6%; Score 27.8; DB 3; Length 6835;
Best Local Similarity 82.1%; Pred. No. 0.93;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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US-09-949-016-16723
; Sequence 16723, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEROF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16723
; LENGTH: 157822
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16723

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Best Local Similarity 96.4%; Pred. No. 6.8;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 4

US-09-125-635-9
; Sequence 9, Application US/09125635
; Patent No. 6562589

GENERAL INFORMATION:

; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4621
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (110)..(4318)
US-09-125-635-9

Query Match 52.4%; Score 26.2; DB 3; Length 4621;
Best Local Similarity 79.5%; Pred. No. 3.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OM nucleic - nucleic search, using sw model

Run on: March 7, 2007, 14:51:58 ; Search time 481 Seconds
(without alignments)

604.921 Million cell updates/sec

Title: US-10-751-113-3

Perfect score: 50
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Total number of hits satisfying chosen parameters: 22169850

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	27.8	55.6	7923	14	US-11-283-329-155	Sequence 155, App
3	27.8	55.6	7935	14	US-11-266-748A-56675	Sequence 56675, A
4	27.8	55.6	7935	14	US-11-283-329-153	Sequence 153, App
5	27.6	55.2	1021	5	US-09-815-264-102471	Sequence 102471, A
6	27.6	55.2	1021	13	US-11-491-125A-41741	Sequence 41741, A
7	27.6	55.2	1052	5	US-09-815-264-16074	Sequence 16074, A
8	27.6	55.2	1113	5	US-09-815-264-40949	Sequence 40949, A
9	27.6	55.2	1415	5	US-09-815-264-73061	Sequence 73061, A
10	27.6	55.2	1415	13	US-11-491-125A-59555	Sequence 59555, A
11	27.6	55.2	1501	5	US-09-815-264-16262	Sequence 16262, A
12	27.6	55.2	1501	5	US-09-815-264-17389	Sequence 17389, A
13	27.6	55.2	1742	5	US-09-815-264-73078	Sequence 73078, A
14	27.6	55.2	1742	13	US-11-491-125A-54764	Sequence 54764, A
15	27.6	55.2	3206	13	US-11-491-125A-24151	Sequence 24151, A
16	27.6	55.2	4056	5	US-09-815-264-67843	Sequence 67843, A
17	27.6	55.2	4056	13	US-11-491-125A-29558	Sequence 29558, A
18	27.6	55.2	5747	13	US-11-491-125A-32347	Sequence 32347, A
19	27.6	55.2	6347	13	US-11-491-125A-46121	Sequence 46121, A
20	27.6	55.2	7819	5	US-09-815-264-70329	Sequence 70329, A
21	27.6	55.2	7819	13	US-11-491-125A-28595	Sequence 28595, A
22	27.6	55.2	15173	5	US-09-815-264-57772	Sequence 57772, A
23	27.6	55.2	15173	13	US-11-491-125A-38938	Sequence 38938, A
24	27.6	55.2	17359	13	US-11-491-125A-41656	Sequence 41656, A
25	27.6	55.2	17450	5	US-09-815-264-75824	Sequence 75824, A
26	27.6	55.2	19831	5	US-09-815-264-61400	Sequence 61400, A
27	27.6	55.2	19831	13	US-11-491-125A-21915	Sequence 21915, A
28	27.6	55.2	23604	5	US-09-815-264-70240	Sequence 70240, A
29	27.6	55.2	23605	13	US-11-491-125A-34250	Sequence 34250, A
30	27.6	55.2	25882	5	US-09-815-264-69888	Sequence 69888, A
31	27.6	55.2	30100	13	US-11-491-125A-26230	Sequence 26230, A
32	27.6	55.2	33842	5	US-09-815-264-59918	Sequence 59918, A
33	27.6	55.2	33842	13	US-11-491-125A-20056	Sequence 20056, A
34	27.6	55.2	42163	5	US-09-815-264-65963	Sequence 65963, A
35	27.6	55.2	42163	13	US-11-491-125A-39406	Sequence 39406, A
36	27.6	55.2	44601	5	US-09-815-264-74332	Sequence 74332, A
37	26.4	52.8	157822	7	US-10-940-774-16723	Sequence 16723, A
38	26	52.0	3718	13	US-11-491-125A-31020	Sequence 31020, A
39	26	52.0	14959	13	US-11-491-125A-9660	Sequence 9660, Ap
40	26	52.0	20779	13	US-11-491-125A-12582	Sequence 12582, A
41	25.2	50.4	20784	5	US-09-815-264-63140	Sequence 63140, A
42	25.2	50.4	789	14	US-11-266-748A-113927	Sequence 113927, A
43	25.2	50.4	789	14	US-11-266-748A-161615	Sequence 161615, A
44	24.6	49.2	5298	13	US-11-491-125A-58886	Sequence 58886, A
45	24.6	49.2	22244	13	US-11-491-125A-42217	Sequence 42217, A

ALIGNMENTS

RESULT 1
US-10-940-774-4981
; Sequence 4981, Application US/10940774
; Publication No. US20070037165A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/10/940,774
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4981
; LENGTH: 6760
; TYPE: DNA
; ORGANISM: Human
US-10-940-774-4981

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Best Local Similarity 82.1%; Pred. No. 6.4;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB      424 AATTAAGGCGAGGAGAAACTATTTCATGATGATGA 462

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US-11-283-329-155
; Sequence 155, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
; FILE REFERENCE: ACADIA-043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 7923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)...(4468)
; OTHER INFORMATION: SRC-3 variant 2
US-11-283-329-155

Query Match      55.6%; Score 27.8; DB 14; Length 7923;
Best Local Similarity 82.1%; Pred. No. 6.5;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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DB      448 AATTAAGGCGAGGAGAAACTATTTCATGATGATGA 486

RESULT 3
US-11-266-748A-56675
; Sequence 56675, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56675
; LENGTH: 7935
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56675

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Best Local Similarity 82.1%; Pred. No. 6.5;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB      448 AATTAAGGCGAGGAGAAACTATTTCATGATGATGA 486

RESULT 4
US-11-283-329-153
; Sequence 153, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
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